

WEST Search History

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DATE: Tuesday, April 26, 2005

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<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L1	scatter\$ diagram	482
<input type="checkbox"/>	L2	L1 same array	14
<input type="checkbox"/>	L3	L2 and gene expression	2
<input type="checkbox"/>	L4	L2 and (mRNA or expression sequence tag or EST)	1
<input type="checkbox"/>	L5	l1 and (high density near \$array\$)	0
<input type="checkbox"/>	L6	(high density near \$array\$)	5166
<input type="checkbox"/>	L7	l6 and l1	0
<input type="checkbox"/>	L8	l1 and (microarray or array or microchip or biochip or chip)	185
<input type="checkbox"/>	L9	L8 and (gene expression or expression level or expression)	67
<input type="checkbox"/>	L10	L9 and (mRNA or EST or expression sequence tag)	12
<input type="checkbox"/>	L11	L10 and event	8
<input type="checkbox"/>	L12	L10 and (event or occurrence)	8
<input type="checkbox"/>	L13	10094407	2
<input type="checkbox"/>	L14	10042407	4
<input type="checkbox"/>	L15	L14 and scatter diagram	0
<input type="checkbox"/>	L16	10/042407	1
<input type="checkbox"/>	L17	L16 and scatter diagram	0
<input type="checkbox"/>	L18	5990078.pn.	2
<input type="checkbox"/>	L19	L16 and (database near search)	1
<input type="checkbox"/>	L20	L16 and (scatter near diagram)	0
<input type="checkbox"/>	L21	L16 and (scatter\$ near diagram)	0
<input type="checkbox"/>	L22	L16 and (changes near expression)	1
<input type="checkbox"/>	L23	Scatter plot or scatter diagram	1871
<input type="checkbox"/>	L24	L23 and (microarray or microchip or chip or biochip or array)	936
<input type="checkbox"/>	L25	L24 and (expression level or gene expression or (expression near level))	340
<input type="checkbox"/>	L26	L25 and (mRNA or est or express\$ sequence tag)	280
<input type="checkbox"/>	L27	L26 and (response same (event or occurrence))	46
<input type="checkbox"/>	L28	L27 and localiz\$	38
<input type="checkbox"/>	L29	L28 and (tissues or cells)	38
<input type="checkbox"/>	L30	L29 and (drug near development)	14

<input type="checkbox"/>	L31	L29 and (probe same hybridiz\$)	28
<input type="checkbox"/>	L32	I27 and (screen\$ near gene\$)	5
<i>DB=PGPB,USPT,USOC,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L33	screen\$ near genes	7073
<input type="checkbox"/>	L34	screen\$ near gene	7073
<input type="checkbox"/>	L35	(screen\$ near gene) same (in situ hybridization)	5
<input type="checkbox"/>	L36	L34 same hybridization	1089
<input type="checkbox"/>	L37	L36 and (probe same (mRNA or express\$ seqenc\$ tag or EST))	593
<input type="checkbox"/>	L38	L37 and (product near (gene expression))	0
<input type="checkbox"/>	L39	L38 and (product same (gene expression))	0
<input type="checkbox"/>	L40	L37 and (product same (gene expression))	281
<input type="checkbox"/>	L41	L40 and (DNA chip or DNA microarray or microarray or microchip or chip)	87
<input type="checkbox"/>	L42	L41 and localization	60
<input type="checkbox"/>	L43	(probe same mRNA) same (in situ hybridization)	835
<input type="checkbox"/>	L44	L43 and (EST or exprress\$ sequence tag or mRNA)	835
<input type="checkbox"/>	L45	L44 and (Localization same mRNA)	368
<input type="checkbox"/>	L46	L45 and (different\$ tissue or different cell)	123
<input type="checkbox"/>	L47	L46 and (DNA chip or DNA microarray or microarray or microchip or chip)	62
<input type="checkbox"/>	L48	(localization near mRNA) or (localization near (express\$ sequence tag or EST))	408
<input type="checkbox"/>	L49	L48 and (in situ hybridization)	164
<input type="checkbox"/>	L50	L49 and (probe near (specifically hybriz\$) near mRNA)	0
<input type="checkbox"/>	L51	L49 and (probe near mRNA)	38
<i>DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L52	screening near genes	2187
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<input type="checkbox"/>	L54	L52 and in situ hybridization	114
<input type="checkbox"/>	L55	L54 and (mRNA localization)	0
<input type="checkbox"/>	L56	L54 and (gene near unknown near function)	1
<input type="checkbox"/>	L57	L54 and (DNA chip or DNA microarray or microarray or microchip or chip)	55
<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L58	L54 and (gene near unknown near function)	1
<input type="checkbox"/>	L59	(screening near gene) and (gene near unknown near function)	59
<input type="checkbox"/>	L60	(screening near gene) same (gene near unknown near function)	5
<input type="checkbox"/>	L61	L60 and in situ hybridization	0
<input type="checkbox"/>	L62	L60 and hybridization	1

<input type="checkbox"/>	L63	insitu hybridization and hybridization	32
<input type="checkbox"/>	L64	insitu hybridization and L59	0
<input type="checkbox"/>	L65	L59 and (hybridization or FISH)	0
<input type="checkbox"/>	L66	L65 and hybridization	0
<input type="checkbox"/>	L67	L59 and hybridization	53
<input type="checkbox"/>	L68	L67 and epression level	0
<input type="checkbox"/>	L69	L67 and expression level	34
<input type="checkbox"/>	L70	L69 and (EST or express\$ sequence tag)	14
<input type="checkbox"/>	L71	L70 and (increase\$ or decrease\$ or chang\$ or modulat\$)	14
<input type="checkbox"/>	L72	(Screening near gene)	4855
<input type="checkbox"/>	L73	L33 same (unknown near function)	22
<input type="checkbox"/>	L74	L73 and differential display	2
<input type="checkbox"/>	L75	L73 and hybridization	11
<input type="checkbox"/>	L76	L73 and (expressed sequence tag or EST)	5
<input type="checkbox"/>	L77	L76 and @pd > 20040823	1

END OF SEARCH HISTORY

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<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L1	6342495.pn.	2
<input type="checkbox"/>	L2	L1 and (scatter near plot or scatter near diagram)	0
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<input type="checkbox"/>	L4	in situ hybridization	6847
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<input type="checkbox"/>	L7	l6 and (event or occurance)	2
<input type="checkbox"/>	L8	L7 and (EST or mRNA or expression sequence tag)	2
<input type="checkbox"/>	L9	l8 and (unknown or unannotat\$)	2
<input type="checkbox"/>	L10	L9 and (before and after)	2
<input type="checkbox"/>	L11	6342495.pn. and scatter	0
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<input type="checkbox"/>	L14	L13 and scatter	0
<input type="checkbox"/>	L15	L13 and scattered	0
<input type="checkbox"/>	L16	L13 and scatter\$	1

END OF SEARCH HISTORY

Identifying genes specifically expressed in different cells of a tissue type for producing cell-specific gene expression profiles in a brain, comprises uses of a polynucleotide **microarray**; brain cell-associated gene expression identification, DNA array and expression profiling useful for drug screening and disease therapy

AUTHOR: BONAVVENTURE P; QUO J; LIU X; KAMME F; MEURERS B; LEYSEN J; BAKKER M

PATENT ASSIGNEE: ORTHO-MCNEIL PHARM INC

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LANGUAGE: English

OTHER SOURCE: WPI: 2002-340114 [37]

AN 2002-12864 BIOTECHDS

AB DERWENT ABSTRACT:

NOVELTY - A polynucleotide **microarray** method comprises at least one polynucleotide as fully defined in the specification, where the expression of polynucleotides is either increased or decreased in brain cells in a response to stress compared to normal brain cells, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) screening a compound for effectiveness in altering expression of target polynucleotides fully defined in the specification, where the polynucleotide expression is either increased or decreased in brain cells in response to stress compared to normal brain cells; and (2) treating depression in a mammal comprises administering a compound identified in (1).

WIDER DISCLOSURE - Also disclosed are following: (1) gene expression profiles produced at a cellular level of multiple brain nuclei after Chronic Mild Stress (CMS) +/- chronic treatment with antidepressant imipramine; (2) a new putative antidepressant was tested to determine whether it has different in-vitro pharmacological properties, but similar behavioural effects of imipramine; and (3) potential new targets for drug discovery to identify compounds useful to treat depression and other neurological diseases and/or conditions.

USE - The new method uses **microarray** technology to identify genes specifically expressed in different cells of a tissue type. Hence, using this method, a catalogue of cell specific gene expression profiles or patterns that can be used to determine which genes are expressed and where in the adult rat brain or central nervous system is provided. In addition, gene expression profiling of selected brain nuclei may help to elucidate the chronic mechanism of antidepressant action and may help to provide a treatment for depression (claimed).

EXAMPLE - Total RNA extraction was carried out in a small volume (20microl/LCM sample) of denaturing buffer, containing 2-mercaptoethanol (10microl/ml) and polyinosine (300ng) were used. The samples were incubated at 42degreesC for 10 minutes and rinsed twice with 500microl Rnase-free water and centrifuged. A cDNA **microarray** containing 2147 cDNA clones was used in this study. All clones were printed as two independent spots on a given chip. A contact pin **microarray** was used to spot the clones in duplicate. Microarrays were hybridized and scanned with a confocal laser scanner. Each **microarray** was normalized at the 75 percentile. Intensity of each clone in the sample was determined as the average of the intensities on the two identical chips. The pair-wise similarity of gene expression profiles within a group of same samples was examined by scatter-plot and the correlation co-efficient was calculated. (89 pages)

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